

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Evans, Mark J.

Matis, Louis A.

Mueller, Eileen Elliott

Nye, Steven H.

Rollins, Scott

Rother, Russell P.

Springhorn, Jeremy P.

Squinto, Stephen P.

Thomas, Thomas C.

~~Wang, Yi~~

Wilkins, James A.

(ii) TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR THE TREATMENT
OF GLOMERULONEPHRITIS AND OTHER INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Maurice M. Klee

(B) STREET: 1951 Burr Street

(C) CITY: Fairfield

(D) STATE: Connecticut

(E) COUNTRY: USA

(F) ZIP: 06430

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.4Mb storage

(B) COMPUTER: Macintosh Cetris 610

(C) OPERATING SYSTEM: System 7

(D) SOFTWARE: WordPerfect 3.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/236,208

(B) FILING DATE: 02-MAY-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Klee, Maurice M.

(B) REGISTRATION NUMBER: 30,399

(C) REFERENCE/DOCKET NUMBER: ALX-138

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (203) 255-1400

(B) TELEFAX: (203) 254-1101

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(A) DESCRIPTION: KSSKC peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Ile Asp His Gln Gly Thr Lys Ser Ser
5 10

Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
15 20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

99

- (A) LENGTH: 1658 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(A) DESCRIPTION: Pro-C5 Polypeptide

(iii) HYPOTHETICAL: No

(iv) ANTIISENSE: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Haviland, D.L.
Haviland, J.C.
Fleischer, D.T.
Hunt, A.
Wetsel, R.A.

(B) TITLE: Complete cDNA Sequence of Human
Complement Pro-C5

(C) JOURNAL: Journal of Immunology

(D) VOLUME: 146

(F) PAGES: 362-368

(G) DATE: 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Leu Leu Gly Ile Leu Cys Phe Leu
-15 -10

Ile Phe Leu Gly Lys Thr Trp Gly Gln Glu Gln Thr Tyr Val
-5 -1 5

Ile Ser Ala Pro Lys Ile Phe Arg Val Gly Ala Ser Glu Asn
10 15 20

Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe Asp Ala

25

30

Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr
35 40 45

Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln
50 55 60

Asn Ser Ala Ile Leu Thr Ile Gln Pro Lys Gln Leu Pro Gly
65 70 75

Gly Gln Asn Pro Val Ser Tyr Val Tyr Leu Glu Val Val Ser
80 85 90

Lys His Phe Ser Lys Ser Lys Arg Met Pro Ile Thr Tyr Asp
95 100

Asn Gly Phe Leu Phe Ile His Thr Asp Lys Pro Val Tyr Thr
105 110 115

Pro Asp Gln Ser Val Lys Val Arg Val Tyr Ser Leu Asn Asp
120 125 130

Asp Leu Lys Pro Ala Lys Arg Glu Thr Val Leu Thr Phe Ile
135 140 145

Asp Pro Glu Gly Ser Glu Val Asp Met Val Glu Glu Ile Asp
150 155 160

His Ile Gly Ile Ile Ser Phe Pro Asp Phe Lys Ile Pro Ser
165 170

Asn Pro Arg Tyr Gly Met Trp Thr Ile Lys Ala Lys Tyr Lys
175 180 185

Glu Asp Phe Ser Thr Thr Gly Thr Ala Tyr Phe Glu Val Lys

101

190							195						200
Glu	Tyr	Val	Leu	Pro	His	Phe	Ser	Val	Ser	Ile	Glu	Pro	Glu
		205					210					215	
Tyr	Asn	Phe	Ile	Gly	Tyr	Lys	Asn	Phe	Lys	Asn	Phe	Glu	Ile
			220					225					230
Thr	Ile	Lys	Ala	Arg	Tyr	Phe	Tyr	Asn	Lys	Val	Val	Thr	Glu
				235						240			
Ala	Asp	Val	Tyr	Ile	Thr	Phe	Gly	Ile	Arg	Glu	Asp	Leu	Lys
245					250						255		
Asp	Asp	Gln	Lys	Glu	Met	Met	Gln	Thr	Ala	Met	Gln	Asn	Thr
	260						265					270	
Met	Leu	Ile	Asn	Gly	Ile	Ala	Gln	Val	Thr	Phe	Asp	Ser	Glu
		275					280					285	
Thr	Ala	Val	Lys	Glu	Leu	Ser	Tyr	Tyr	Ser	Leu	Glu	Asp	Leu
			290					295					300
Asn	Asn	Lys	Tyr	Leu	Tyr	Ile	Ala	Val	Thr	Val	Ile	Glu	Ser
				305						310			
Thr	Gly	Gly	Phe	Ser	Glu	Glu	Ala	Glu	Ile	Pro	Gly	Ile	Lys
315					320					325			
Tyr	Val	Leu	Ser	Pro	Tyr	Lys	Leu	Asn	Leu	Val	Ala	Thr	Pro
	330					335					340		
Leu	Phe	Leu	Lys	Pro	Gly	Ile	Pro	Tyr	Pro	Ile	Lys	Val	Gln
		345					350					355	
Val	Lys	Asp	Ser	Leu	Asp	Gln	Leu	Val	Gly	Gly	Val	Pro	Val

				360					365					370
Ile	Leu	Asn	Ala	Gln	Thr	Ile	Asp	Val	Asn	Gln	Glu	Thr	Ser	
				375					380					
Asp	Leu	Asp	Pro	Ser	Lys	Ser	Val	Thr	Arg	Val	Asp	Asp	Gly	
385					390					395				
Val	Ala	Ser	Phe	Val	Leu	Asn	Leu	Pro	Ser	Gly	Val	Thr	Val	
	400					405					410			
Leu	Glu	Phe	Asn	Val	Lys	Thr	Asp	Ala	Pro	Asp	Leu	Pro	Glu	
		415					420					425		
Glu	Asn	Gln	Ala	Arg	Glu	Gly	Tyr	Arg	Ala	Ile	Ala	Tyr	Ser	
			430					435					440	
Ser	Leu	Ser	Gln	Ser	Tyr	Leu	Tyr	Ile	Asp	Trp	Thr	Asp	Asn	
				445					450					
His	Lys	Ala	Leu	Leu	Val	Gly	Glu	His	Leu	Asn	Ile	Ile	Val	
455					460					465				
Thr	Pro	Lys	Ser	Pro	Tyr	Ile	Asp	Lys	Ile	Thr	His	Tyr	Asn	
	470					475					480			
Tyr	Leu	Ile	Leu	Ser	Lys	Gly	Lys	Ile	Ile	His	Phe	Gly	Thr	
		485					490					495		
Arg	Glu	Lys	Phe	Ser	Asp	Ala	Ser	Tyr	Gln	Ser	Ile	Asn	Ile	
			500					505					510	
Pro	Val	Thr	Gln	Asn	Met	Val	Pro	Ser	Ser	Arg	Leu	Leu	Val	
				515					520					
Tyr	Tyr	Ile	Val	Thr	Gly	Glu	Gln	Thr	Ala	Glu	Leu	Val	Ser	

103

525					530						535			
Asp	Ser	Val	Trp	Leu	Asn	Ile	Glu	Glu	Lys	Cys	Gly	Asn	Gln	
540						545					550			
Leu	Gln	Val	His	Leu	Ser	Pro	Asp	Ala	Asp	Ala	Tyr	Ser	Pro	
	555						560					565		
Gly	Gln	Thr	Val	Ser	Leu	Asn	Met	Ala	Thr	Gly	Met	Asp	Ser	
		570						575					580	
Trp	Val	Ala	Leu	Ala	Ala	Val	Asp	Ser	Ala	Val	Tyr	Gly	Val	
			585						590					
Gln	Arg	Gly	Ala	Lys	Lys	Pro	Leu	Glu	Arg	Val	Phe	Gln	Phe	
595					600					605				
Leu	Glu	Lys	Ser	Asp	Leu	Gly	Cys	Gly	Ala	Gly	Gly	Gly	Leu	
	610					615					620			
Asn	Asn	Ala	Asn	Val	Phe	His	Leu	Ala	Gly	Leu	Thr	Phe	Leu	
	625						630					635		
Thr	Asn	Ala	Asn	Ala	Asp	Asp	Ser	Gln	Glu	Asn	Asp	Glu	Pro	
		640						645					650	
Cys	Lys	Glu	Ile	Leu	Arg	Pro	Arg	Arg	Thr	Leu	Gln	Lys	Lys	
			655						660					
Ile	Glu	Glu	Ile	Ala	Ala	Lys	Tyr	Lys	His	Ser	Val	Val	Lys	
665				670						675				
Lys	Cys	Cys	Tyr	Asp	Gly	Ala	Cys	Val	Asn	Asn	Asp	Glu	Thr	
	680					685					690			
Cys	Glu	Gln	Arg	Ala	Ala	Arg	Ile	Ser	Leu	Gly	Pro	Arg	Cys	

695	700	705
Ile Lys Ala Phe Thr Glu Cys Cys Val Val Ala Ser Gln Leu		
710	715	720
Arg Ala Asn Ile Ser His Lys Asp Met Gln Leu Gly Arg Leu		
725	730	
His Met Lys Thr Leu Leu Pro Val Ser Lys Pro Glu Ile Arg		
735	740	745
Ser Tyr Phe Pro Glu Ser Trp Leu Trp Glu Val His Leu Val		
750	755	760
Pro Arg Arg Lys Gln Leu Gln Phe Ala Leu Pro Asp Ser Leu		
765	770	775
Thr Thr Trp Glu Ile Gln Gly Ile Gly Ile Ser Asn Thr Gly		
780	785	790
Ile Cys Val Ala Asp Thr Val Lys Ala Lys Val Phe Lys Asp		
795	800	
Val Phe Leu Glu Met Asn Ile Pro Tyr Ser Val Val Arg Gly		
805	810	815
Glu Gln Ile Gln Leu Lys Gly Thr Val Tyr Asn Tyr Arg Thr		
820	825	830
Ser Gly Met Gln Phe Cys Val Lys Met Ser Ala Val Glu Gly		
835	840	845
Ile Cys Thr Ser Glu Ser Pro Val Ile Asp His Gln Gly Thr		
850	855	860

Lys Ser Ser Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
865 870

Ser His Leu Val Thr Phe Thr Val Leu Pro Leu Glu Ile Gly
875 880 885

Leu His Asn Ile Asn Phe Ser Leu Glu Thr Trp Phe Gly Lys
890 895 900

Glu Ile Leu Val Lys Thr Leu Arg Val Val Pro Glu Gly Val
905 910 915

Lys Arg Glu Ser Tyr Ser Gly Val Thr Leu Asp Pro Arg Gly
920 925 930

Ile Tyr Gly Thr Ile Ser Arg Arg Lys Glu Phe Pro Tyr Arg
935 940

Ile Pro Leu Asp Leu Val Pro Lys Thr Glu Ile Lys Arg Ile
945 950 955

Leu Ser Val Lys Gly Leu Leu Val Gly Glu Ile Leu Ser Ala
960 965 970

Val Leu Ser Gln Glu Gly Ile Asn Ile Leu Thr His Leu Pro
975 980 985

Lys Gly Ser Ala Glu Ala Glu Leu Met Ser Val Val Pro Val
990 995 1000

Phe Tyr Val Phe His Tyr Leu Glu Thr Gly Asn His Trp Asn
1005 1010

Ile Phe His Ser Asp Pro Leu Ile Glu Lys Gln Lys Leu Lys
1015 1020 1025

Lys Lys Leu Lys Glu Gly Met Leu Ser Ile Met Ser Tyr Arg
1030 1035 1040

Asn Ala Asp Tyr Ser Tyr Ser Val Trp Lys Gly Gly Ser Ala
1045 1050 1055

Ser Thr Trp Leu Thr Ala Phe Ala Leu Arg Val Leu Gly Gln
1060 1065 1070

Val Asn Lys Tyr Val Glu Gln Asn Gln Asn Ser Ile Cys Asn
1075 1080

Ser Leu Leu Trp Leu Val Glu Asn Tyr Gln Leu Asp Asn Gly
1085 1090 1095

Ser Phe Lys Glu Asn Ser Gln Tyr Gln Pro Ile Lys Leu Gln
1100 1105 1110

Gly Thr Leu Pro Val Glu Ala Arg Glu Asn Ser Leu Tyr Leu
1115 1120 1125

Thr Ala Phe Thr Val Ile Gly Ile Arg Lys Ala Phe Asp Ile
1130 1135 1140

Cys Pro Leu Val Lys Ile Asp Thr Ala Leu Ile Lys Ala Asp
1145 1150

Asn Phe Leu Leu Glu Asn Thr Leu Pro Ala Gln Ser Thr Phe
1155 1160 1165

Thr Leu Ala Ile Ser Ala Tyr Ala Leu Ser Leu Gly Asp Lys
1170 1175 1180

Thr His Pro Gln Phe Arg Ser Ile Val Ser Ala Leu Lys Arg
1185 1190 1195

Glu Ala Leu Val Lys Gly Asn Pro Pro Ile Tyr Arg Phe Trp
1200 1205 1210

Lys Asp Asn Leu Gln His Lys Asp Ser Ser Val Pro Asn Thr
1215 1220

Gly Thr Ala Arg Met Val Glu Thr Thr Ala Tyr Ala Leu Leu
1225 1230 1235

Thr Ser Leu Asn Leu Lys Asp Ile Asn Tyr Val Asn Pro Val
1240 1245 1250

Ile Lys Trp Leu Ser Glu Glu Gln Arg Tyr Gly Gly Gly Phe
1255 1260 1265

Tyr Ser Thr Gln Asp Thr Ile Asn Ala Ile Glu Gly Leu Thr
1270 1275 1280

Glu Tyr Ser Leu Leu Val Lys Gln Leu Arg Leu Ser Met Asp
1285 1290

Ile Asp Val Ser Tyr Lys His Lys Gly Ala Leu His Asn Tyr
1295 1300 1305

Lys Met Thr Asp Lys Asn Phe Leu Gly Arg Pro Val Glu Val
1310 1315 1320

Leu Leu Asn Asp Asp Leu Ile Val Ser Thr Gly Phe Gly Ser
1325 1330 1335

Gly Leu Ala Thr Val His Val Thr Thr Val Val His Lys Thr
1340 1345 1350

Ser Thr Ser Glu Glu Val Cys Ser Phe Tyr Leu Lys Ile Asp
1355 1360

Thr Gln Asp Ile Glu Ala Ser His Tyr Arg Gly Tyr Gly Asn
1365 1370 1375

Ser Asp Tyr Lys Arg Ile Val Ala Cys Ala Ser Tyr Lys Pro
1380 1385 1390

Ser Arg Glu Glu Ser Ser Ser Gly Ser Ser His Ala Val Met
1395 1400 1405

Asp Ile Ser Leu Pro Thr Gly Ile Ser Ala Asn Glu Glu Asp
1410 1415 1420

Leu Lys Ala Leu Val Glu Gly Val Asp Gln Leu Phe Thr Asp
1425 1430

Tyr Gln Ile Lys Asp Gly His Val Ile Leu Gln Leu Asn Ser
1435 1440 1445

Ile Pro Ser Ser Asp Phe Leu Cys Val Arg Phe Arg Ile Phe
1450 1455 1460

Glu Leu Phe Glu Val Gly Phe Leu Ser Pro Ala Thr Phe Thr
1465 1470 1475

Val Tyr Glu Tyr His Arg Pro Asp Lys Gln Cys Thr Met Phe
1480 1485 1490

Tyr Ser Thr Ser Asn Ile Lys Ile Gln Lys Val Cys Glu Gly
1495 1500

Ala Ala Cys Lys Cys Val Glu Ala Asp Cys Gly Gln Met Gln
1505 1510 1515

Glu Glu Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln
1520 1525 1530

Thr Ala Cys Lys Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ser
1535 1540 1545

Ile Thr Ser Ile Thr Val Glu Asn Val Phe Val Lys Tyr Lys
1550 1555 1560

Ala Thr Leu Leu Asp Ile Tyr Lys Thr Gly Glu Ala Val Ala
1565 1570

Glu Lys Asp Ser Glu Ile Thr Phe Ile Lys Lys Val Thr Cys
1575 1580 1585

Thr Asn Ala Glu Leu Val Lys Gly Arg Gln Tyr Leu Ile Met
1590 1595 1600

Gly Lys Glu Ala Leu Gln Ile Lys Tyr Asn Phe Ser Phe Arg
1605 1610 1615

Tyr Ile Tyr Pro Leu Asp Ser Leu Thr Trp Ile Glu Tyr Trp
1620 1625 1630

Pro Arg Asp Thr Thr Cys Ser Ser Cys Gln Ala Phe Leu Ala
1635 1640

Asn Leu Asp Glu Phe Ala Glu Asp Ile Phe Leu Asn Gly Cys
1645 1650 1655

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4059 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Apex-1 Eukaryotic
Expression Vector

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACGCGTTGAC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG	50
GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACTTACGG	100
TAAATGGCCC CGCCTGGCTG ACCGCCCAAC GACCCCCGCC CATTGACGTC	150
AATAATGACG TATGTTCCCA TAGTAACGCC AATAGGGACT TTCCATTGAC	200
GTCAATGGGT GGACTATTTA CGGTAAACTG CCCACTTGGC AGTACATCAA	250
GTGTATCATA TGCCAAGTAC GCCCCCTATT GACGTCAATG ACGGTAAATG	300
GCCCGCCTGG CATTATGCCC AGTACATGAC CTTATGGGAC TTCCTACTT	350
GGCAGTACAT CTACGTATTA GTCATCGCTA TTACCATGGT GATGCGGTTT	400
TGGCAGTACA TCAATGGGCG TGGATAGCGG TTTGACTCAC GGGGATTTCC	450
AAGTCTCCAC CCCATTGACG TCAATGGGAG TTTGTTTTGG CACCAAATC	500
AACGGGACTT TCCAAAATGT CGTAACAACT CCGCCCCATT GACGCAAATG	550
GGCGGTAGGC GTGTACGGTG GGAGGTCTAT ATAAGCAGAG CTCGTTTAGT	600
GAACCGTCAG AATTCTGTTG GGCTCGCGGT TGATTACAAA CTCTTCGCGG	650
TCTTTCCAGT ACTCTTGGAT CGGAAACCCG TCGGCCTCCG AACGGTACTC	700
CGCCACCGAG GGACCTGAGC GAGTCCGCAT CGACCGGATC GGAAAACCTC	750

TCGACTGTTG GGGTGAGTAC TCCCTCTCAA AAGCGGGCAT GACTTCTGCG	800
CTAAGATTGT CAGTTTCCAA AAACGAGGAG GATTTGATAT TCACCTGGCC	850
CGCGGTGATG CCTTTGAGGG TGGCCGCGTC CATCTGGTCA GAAAAGACAA	900
TCTTTTTTGT GTCAAGCTTG AGGTGTGGCA GGCTTGAGAT CTGGCCATAC	950
ACTTGAGTGA CAATGACATC CACTTTGCCT TTCTCTCCAC AGGTGTCCAC	1000
TCCCAGGTCC AACTGCAGGT CGACCGGCTT GGTACCGAGC TCGGATCCAC	1050
TAGTAACGGC CGCCAGTGTG CTGGAATTCT GCAGATATCC ATCACACTGG	1100
CGGCCGCTCG AGCATGCATC TAGAACTTGT TTATTGCAGC TTATAATGGT	1150
TACAAATAAA GCAATAGCAT CACAAATTC ACAAATAAAG CATTTTTTTC	1200
ACTGCATTCT AGTTGTGGTT TGTCCAAACT CATCAATGTA TCTTATCATG	1250
TCTGGATCGA TCCCGCCATG GTATCAACGC CATATTTCTA TTTACAGTAG	1300
GGACCTCTTC GTTGTGTAGG TACCGCTGTA TTCCTAGGGA AATAGTAGAG	1350
GCACCTTGAA CTGTCTGCAT CAGCCATATA GCCCCGCTG TTCGACTTAC	1400
AAACACAGGC ACAGTACTGA CAAACCCATA CACCTCCTCT GAAATACCCA	1450
TAGTTGCTAG GGCTGTCTCC GAACTCATTA CACCCTCCAA AGTCAGAGCT	1500
GTAATTTTCG CATCAAGGGC AGCGAGGGCT TCTCCAGATA AAATAGCTTC	1550
TGCCGAGAGT CCCGTAAGGG TAGACACTTC AGCTAATCCC TCGATGAGGT	1600
CTACTAGAAT AGTCAGTGCG GCTCCCATTT TGAAAATTCA CTTACTTGAT	1650

CAGCTTCAGA AGATGGCGGA GGGCCTCCAA CACAGTAATT TTCCTCCCGA	1700
CTCTTAAAAT AGAAAATGTC AAGTCAGTTA AGCAGGAAGT GGAATAACTG	1750
ACGCAGCTGG CCGTGCGACA TCCTCTTTTA ATTAGTTGCT AGGCAACGCC	1800
CTCCAGAGGG CGTGTGGTTT TGCAAGAGGA AGCAAAAGCC TCTCCACCCA	1850
GGCCTAGAAT GTTTCACACC AATCATTACT ATGACAACAG CTGTTTTTTT	1900
TAGTATTAAG CAGAGGCCGG GGACCCCTGG GCCCGCTTAC TCTGGAGAAA	1950
AAGAAGAGAG GCATTGTAGA GGCTTCCAGA GGCAACTTGT CAAAACAGGA	2000
CTGCTTCTAT TTCTGTCACA CTGTCTGGCC CTGTCACAAG GTCCAGCACC	2050
TCCATACCCC CTTTAATAAG CAGTTTGGGA ACGGGTGCGG GTCTTACTCC	2100
GCCCATCCCG CCCCTAACTC CGCCCAGTTC CGCCCATTCT CCGCCCCATG	2150
GCTGACTAAT TTTTTTTATT TATGCAGAGG CCGAGGCCGC CTCGGCCTCT	2200
GAGCTATTCC AGAAGTAGTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG	2250
CAAAAAGGAG CTCCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG	2300
CTGGCGTTTT TCCATAGGCT CCGCCCCCCT GACGAGCATC AAAAAATCG	2350
ACGCTCAAGT CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG	2400
CGTTTCCCCC TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG	2450
CTTACCGGAT ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC	2500
TCAATGCTCA CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA	2550
AGCTGGGCTG TGTGCACGAA CCCCCGTTC AGCCCGACCG CTGCGCCTTA	2600

TCCGGTAACT ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC	2650
ACTGGCAGCA GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG	2700
GTGCTACAGA GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAGG	2750
ACAGTATTTG GTATCTGCGC TCTGCTGAAG CCAGTTACCT TCGGAAAAAG	2800
AGTTGGTAGC TCTTGATCCG GCAAACAAAC CACCGCTGGT AGCGGTGGTT	2850
TTTTTGTTTG CAAGCAGCAG ATTACGCGCA GAAAAAAGG ATCTCAAGAA	2900
GATCCTTTGA TCTTTTCTAC GGGGTCTGAC GCTCAGTGGA ACGAAACTC	2950
ACGTTAAGGG ATTTTGGTCA TGAGATTATC AAAAAGGATC TTCACCTAGA	3000
TCCTTTTAAA TTAAAAATGA AGTTTTAAAT CAATCTAAAG TATATATGAG	3050
TAAACTTGGT CTGACAGTTA CCAATGCTTA ATCAGTGAGG CACCTATCTC	3100
AGCGATCTGT CTATTTTCGTT CATCCATAGT TGCCTGACTC CCCGTCGTGT	3150
AGATAACTAC GATACGGGAG GGCTTACCAT CTGGCCCCAG TGCTGCAATG	3200
ATACCGCGAG ACCCACGCTC ACCGGCTCCA GATTTATCAG CAATAAACCA	3250
GCCAGCCGGA AGGGCCGAGC GCAGAAGTGG TCCTGCAACT TTATCCGCCT	3300
CCATCCAGTC TATTAATTGT TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA	3350
GTTAATAGTT TGCGCAACGT TGTTGCCATT GCTACAGGCA TCGTGGTGTC	3400
ACGCTCGTCG TTTGGTATGG CTTCAATCAG CTCCGGTTCC CAACGATCAA	3450
GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC	3500

GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG GCCGCAGTGT TATCACTCAT	3550
GGTTATGGCA GCACTGCATA ATTCTCTTAC TGTCATGCCA TCCGTAAGAT	3600
GCTTTTCTGT GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT	3650
ATGCGGCGAC CGAGTTGCTC TTGCCCCGGCG TCAATACGGG ATAATACCGC	3700
GCCACATAGC AGAACTTTAA AAGTGCTCAT CATTGGAAAA CGTTCTTCGG	3750
GGCGAAAACCT CTCAAGGATC TTACCGCTGT TGAGATCCAG TTCGATGTAA	3800
CCCACCTCGTG CACCCAACCTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT	3850
TTCTGGGTGA GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA	3900
GGGCGACACG GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATATTAT	3950
TGAAGCATTT ATCAGGGTTA TTGTCTCATG AGCGGATACA TATTTGAATG	4000
TATTTAGAAA AATAAACAAA TAGGGGTTC GCGCACATTT CCCCAGAAAAG	4050
TGCCACCTG	4059

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8540 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Apex-3P Eukaryotic
Expression Vector

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGACCAATA	CAAAACAAAA	GCGCCCCTCG	TACCAGCGAA	GAAGGGGCAG	50
AGATGCCGTA	GTCAGGTTTA	GTTTCGTCCGG	CGGCGGGGGA	TCTGTATGGT	100
GCACTCTCAG	TACAATCTGC	TCTGATGCCG	CATAGTTAAG	CCAGTATCTG	150
CTCCCTGCTT	GTGTGTTGGA	GGTCGCTGAG	TAGTGCGCGA	GCAAAATTTA	200
AGCTACAACA	AGGCAAGGCT	TGACCGACAA	TTGCATGAAG	AATCTGCTTA	250
GGGTTAGGCG	TTTTGCGCTG	CTTCGCGATG	TACGGGCCAG	ATATACGCGT	300
TGACATTGAT	TATTGACTAG	TTATTAATAG	TAATCAATTA	CGGGGTCATT	350
AGTTCATAGC	CCATATATGG	AGTTCCGCGT	TACATAACTT	ACGGTAAATG	400
GCCCGCCTGG	CTGACCGCCC	AACGACCCCC	GCCCATTGAC	GTCAATAATG	450
ACGTATGTTC	CCATAGTAAC	GCCAATAGGG	ACTTTCCATT	GACGTCAATG	500
GGTGGACTAT	TTACGGTAAA	CTGCCCCACTT	GGCAGTACAT	CAAGTGTATC	550
ATATGCCAAG	TACGCCCCCT	ATTGACGTCA	ATGACGGTAA	ATGGCCCCGCC	600
TGGCATTATG	CCCAGTACAT	GACCTTATGG	GACTTTCCTA	CTTGGCAGTA	650
CATCTACGTA	TTAGTCATCG	CTATTACCAT	GGTGATGCGG	TTTTGGCAGT	700
ACATCAATGG	GCGTGGATAG	CGGTTTGACT	CACGGGGATT	TCCAAGTCTC	750
CACCCCATTG	ACGTCAATGG	GAGTTTGTTT	TGGCACCAAA	ATCAACGGGA	800

CTTTCCAAAA TGTCGTAACA ACTCCGCCCC ATTGACGCAA ATGGGCGGTA 850
GGCGTGTACG GTGGGAGGTC TATATAAGCA GAGCTCGTTT AGTGAACCGT 900
CAGAATTCTG TTGGGCTCGC GGTTGATTAC AACTCTTCG CGGTCTTTCC 950
AGTACTCTTG GATCGGAAAC CCGTCGGCCT CCGAACGGTA CTCCGCCACC 1000
GAGGGACCTG AGCGAGTCCG CATCGACCGG ATCGGAAAAC CTCTCGACTG 1050
TTGGGGTGAG TACTCCCTCT CAAAAGCGGG CATGACTTCT GCGCTAAGAT 1100
TGTCAGTTTC CAAAACGAG GAGGATTTGA TATTCACCTG GCCCGCGGTG 1150
ATGCCTTTGA GGGTGGCCGC GTCCATCTGG TCAGAAAAGA CAATCTTTTT 1200
GTTGTCAAGC TTGAGGTGTG GCAGGCTTGA GATCTGGCCA TACTCTGAG 1250
TGACAATGAC ATCCACTTTG CCTTTCTCTC CACAGGTGTC CACTCCCAGG 1300
TCCAAGTCA GGTCGACCGG CTTGGTACCG AGCTCGGATC CTCTAGAGTC 1350
GACCTGCAGG CATGCAAGCT TGGCACTGGC CGTCGTTTTA CAACGTCGTG 1400
ACTGGGAAAA CCCTGGCGTT ACCCAACTTA ATCGCCTTGC AGCACATCCC 1450
CCTTTCGCCA GCTGGCGTAA TAGCGAAGAG GCCCGCACCG ATCCAGACAT 1500
GATAAGATAC ATTGATGAGT TTGGACAAAC CACAACTAGA ATGCAGTGAA 1550
AAAAATGCTT TATTTGTGAA ATTTGTGATG CTATTGCTTT ATTTGTAACC 1600
ATTATAAGCT GCAATAAACA AGTTAACAAC AACAATTGCA TTCATTTTAT 1650
GTTTCAGGTT CAGGGGGAGG TGTGGGAGGT TTTTAAAGC AAGTAAAACC 1700

TCTACAAATG TGGTATGGCT GATTATGATC CCCAGGAAGC TCCTCTGTGT 1750
CCTCATAAAC CCTAACCTCC TCTACTTGAG AGGACATTCC AATCATAGGC 1800
TGCCCATCCA CCCTCTGTGT CCTCCTGTTA ATTAGGTCAC TTAACAAAAA 1850
GGAAATTGGG TAGGGGTTTT TCACAGACCG CTTTCTAAGG GTAATTTTAA 1900
AATATCTGGG AAGTCCCTTC CACTGCTGTG TTCCAGAAGT GTTGGTAAAC 1950
AGCCCACAAA TGTCAACAGC AGAAACATAC AAGCTGTCAG CTTTGCACAA 2000
GGGCCCAACA CCCTGCTCAT CAAGAAGCAC TGTGGTTGCT GTGTTAGTAA 2050
TGTGCAAAAC AGGAGGCACA TTTTCCCCAC CTGTGTAGGT TCCAAAATAT 2100
CTAGTGTTTT CATTTTTACT TGGATCAGGA ACCCAGCACT CCACTGGATA 2150
AGCATTATCC TTATCCAAAA CAGCCTTGTG GTCAGTGTTT ATCTGCTGAC 2200
TGTCAACTGT AGCATTTTTT GGGGTTACAG TTTGAGCAGG ATATTTGGTC 2250
CTGTAGTTTG CTAACACACC CTGCAGCTCC AAAGGTCCC CACCAACAGC 2300
AAAAAATGA AAATTTGACC CTTGAATGGG TTTTCCAGCA CCATTTTCAT 2350
GAGTTTTTTG TGTCCCTGAA TGCAAGTTTA ACATAGCAGT TACCCCAATA 2400
ACCTCAGTTT TAACAGTAAC AGCTTCCCAC ATCAAAATAT TTCCACAGGT 2450
TAAGTCCTCA TTTGTAGAAT TCGCCAGCAC AGTGGTCGAC CCTGTGGATG 2500
TGTGTCACTT AGGGTGTGGA AAGTCCCCAG GCTCCCCAGC AGGCAGAAGT 2550
ATGCAAAGCA TGCATCTCAA TTAGTCAGCA ACCAGGTGTG GAAAGTCCCC 2600

AGGCTCCCCA GCAGGCAGAA GTATGCAAAG CATGCATCTC AATTAGTCAG 2650
CAACCATAGT CCCGCCCCTA ACTCCGCCCA TCCCGCCCCT AACTCCGCCC 2700
AGTTCCGCCC ATTCTCCGCC CCATGGCTGA CTAATTTTTT TTATTTATGC 2750
AGAGGCCGAG GCCGCCTCGG CCTCTGAGCT ATTCCAGAAG TAGTGAGGAG 2800
GCTTTTTTGG AGGCCTAGGC TTTTGCAAAA GCTTACCATG ACCGAGTACA 2850
AGCCCACGGT GCGCCTCGCC ACCCGCGACG ACGTCCCCCG GGCCGTACGC 2900
ACCCTCGCCG CCGCGTTCGC CGACTACCCC GCCACGCGCC ACACCGTCGA 2950
CCCGGACCGC CACATCGAGC GGGTCACCGA GCTGCAAGAA CTCTTCCTCA 3000
CGCGCGTCGG GCTCGACATC GGCAAGGTGT GGGTCGCGGA CGACGGCGCC 3050
GCGGTGGCGG TCTGGACCAC GCCGGAGAGC GTCGAAGCGG GGGCGGTGTT 3100
CGCCGAGATC GGCCCGCGCA TGGCCGAGTT GAGCGGTTC CCGCTGGCCG 3150
CGCAGCAACA GATGGAAGGC CTCCTGGCGC CGCACCGGCC CAAGGAGCCC 3200
GCGTGGTTCC TGGCCACCGT CGGCGTCTCG CCCGACCACC AGGGCAAGGG 3250
TCTGGGCAGC GCCGTCGTGC TCCCCGGAGT GGAGGCGGCC GAGCGCGCCG 3300
GGGTGCCCCG CTCCTGGAG ACCTCCGCGC CCCGCAACCT CCCCTTCTAC 3350
GAGCGGCTCG GCTTCACCGT CACCGCCGAC GTCGAGTGCC CGAAGGACCG 3400
CGCGACCTGG TGCATGACCC GCAAGCCCGG TGCCTGACGC CCGCCCCACG 3450
ACCCGCAGCG CCCGACCGAA AGGAGCGCAC GACCCCATGC ATCGATAAAA 3500

TAAAAGATTT TATTTAGTCT CCAGAAAAAG GGGGGAATGA AAGACCCAC 3550
CTGTAGGTTT GGCAAGCTAG AACTTGTTTA TTGCAGCTTA TAATGGTTAC 3600
AAATAAAGCA ATAGCATCAC AAATTCACA AATAAAGCAT TTTTTTCACT 3650
GCATTCTAGT TGTGGTTTGT CCAAACATCAT CAATGTATCT TATCATGTCT 3700
GGATCGATCC CGCCATGGTA TCAACGCCAT ATTTCTATTT ACAGTAGGGA 3750
CCTCTTCGTT GTGTAGGTAC CCCGGGTTCG AAATCGAATT CGCCAATGAC 3800
AAGACGCTGG GCGGGGTTTG TGTCATCATA GAACTAAAGA CATGCAAATA 3850
TATTTCTTCC GGGGACACCG CCAGCAAACG CGAGCAACGG GCCACGGGGA 3900
TGAAGCAGCC CGGCGGCACC TCGCTAACGG ATTCACCACT CCAAGAATTG 3950
GAGCCAATCA ATTCTTGCGG AGAACTGTGA ATGCGCAAAC CAACCCTTGG 4000
CAGAACATAT CCATCGCGTC CGCCATCTCC AGCAGCCGCA CGCGGCGCAT 4050
CTCGGGGCCG ACGCGCTGGG CTACGTCTTG CTGGCGTTTCG CGACGCGAGG 4100
CTGGATGGCC TTCCCCATTA TGATTCTTCT CGCTTCCGGC GGCATCGGGA 4150
TGCCCGCGTT GCAGGCCATG CTGTCCAGGC AGGTAGATGA CGACCATCAG 4200
GGACAGCTTC AAGGATCGCT CGCGGCTCTT ACCAGCGCCA GCAAAGGCC 4250
AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTTCATA GGCTCCGCCC 4300
CCCTGACGAG CATCACAAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC 4350
CGACAGGACT ATAAAGATAC CAGGCGTTTC CCCCTGGAAG CTCCCTCGTG 4400

CGCTCTCCTG TTCCGACCCT GCCGCTTACC GGATACCTGT CCGCCTTTCT 4450
CCCTTCGGGA AGCGTGGCGC TTTCTCATAG CTCACGCTGT AGGTATCTCA 4500
GTTTCGGTGTA GGTCGTTCGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC 4550
GTTTCAGCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA 4600
CCCGGTAAGA CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA 4650
TTAGCAGAGC GAGGTATGTA GGCGGTGCTA CAGAGTTCTT GAAGTGGTGG 4700
CCTAACTACG GCTACACTAG AAGGACAGTA TTTGGTATCT GCGCTCTGCT 4750
GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG TAGCTCTTGA TCCGGCAAAC 4800
AAACCACCGC TGGTAGCGGT GGTTTTTTTG TTTGCAAGCA GCAGATTACG 4850
CGCAGAAAAA AAGGATCTCA AGAAGATCCT TTGATCTTTT CTACGGGGTC 4900
TGACGCTCAG TGGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT 4950
TATCAAAAAG GATCTTCACC TAGATCCTTT TAAATTAAAA ATGAAGTTTT 5000
AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG 5050
CTTAATCAGT GAGGCACCTA TCTCAGCGAT CTGTCTATTT CGTTCATCCA 5100
TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA 5150
CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC GCTCACCGGC 5200
TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA 5250
GTGGTCCTGC AACTTTATCC GCCTCCATCC AGTCTATTAA TTGTTGCCGG 5300

GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC 5350
CATTGCTGCA GGCATCGTGG TGTCACGCTC GTCGTTTGGT ATGGCTTCAT 5400
TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG 5450
TGCAAAAAAG CGGTTAGCTC CTTCGGTCCT CCGATCGTTG TCAGAAGTAA 5500
GTTGGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC 5550
TTACTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTGG TGAGTACTCA 5600
ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC 5650
GGCGTCAACA CGGGATAATA CCGCGCCACA TAGCAGAACT TTAAAAGTGC 5700
TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG 5750
CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC 5800
AGCATCTTTT ACTTTCACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC 5850
AAAATGCCGC AAAAAAGGGA ATAAGGGCGA CACGGAAATG TTGAATACTC 5900
ATACTCTTCC TTTTTC AATA TTATTGAAGC ATTTATCAGG GTTATTGTCT 5950
CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA CAAATAGGGG 6000
TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC CTGACGTCTA AGAAACCATT 6050
ATTATCATGA CATTAACCTA TAAAAATAGG CGTATCACGA GGCCCTTTTCG 6100
TCTTCAAGAA TTCTCATGTT TGACAGCTTA TCGTAGACAT CATGCGTGCT 6150
GTTGGTGTAT TTCTGGCCAT CTGTCTTGTC ACCATTTTCG TCCTCCCAAC 6200

ATGGGGCAAT TGGGCATACC CATGTTGTCA CGTCACTCAG CTCCGCGCTC 6250
AACACCTTCT CGCGTTGGAA AACATTAGCG ACATTTACCT GGTGAGCAAT 6300
CAGACATGCG ACGGCTTTAG CCTGGCCTCC TTAAATTCAC CTAAGAATGG 6350
GAGCAACCAG CAGGAAAAGG ACAAGCAGCG AAAATTCACG CCCCCTTGGG 6400
AGGTGGCGGC ATATGCAAAG GATAGCACTC CCACTCTACT ACTGGGTATC 6450
ATATGCTGAC TGTATATGCA TGAGGATAGC ATATGCTACC CGGATACAGA 6500
TTAGGATAGC ATATACTACC CAGATATAGA TTAGGATAGC ATATGCTACC 6550
CAGATATAGA TTAGGATAGC CTATGCTACC CAGATATAAA TTAGGATAGC 6600
ATATACTACC CAGATATAGA TTAGGATAGC ATATGCTACC CAGATATAGA 6650
TTAGGATAGC CTATGCTACC CAGATATAGA TTAGGATAGC ATATGCTACC 6700
CAGATATAGA TTAGGATAGC ATATGCTATC CAGATATTTG GGTAGTATAT 6750
GCTACCCAGA TATAAATTAG GATAGCATAT ACTACCCTAA TCTCTATTAG 6800
GATAGCATAT GCTACCCGGA TACAGATTAG GATAGCATAT ACTACCCAGA 6850
TATAGATTAG GATAGCATAT GCTACCCAGA TATAGATTAG GATAGCCTAT 6900
GCTACCCAGA TATAAATTAG GATAGCATAT ACTACCAGA TATAGATTAG 6950
GATAGCATAT GCTACCCAGA TATAGATTAG GATAGCCTAT GCTACCCAGA 7000
TATAGATTAG GATAGCATAT GCTATCCAGA TATTTGGGTA GTATATGCTA 7050
CCCATGGCAA CATTAGCCCA CCGTGCTCTC AGCGACCTCG TGAATATGAG 7100

GACCAACAAC CCTGTGCTTG GCGCTCAGGC GCAAGTGTGT GTAATTTGTC 7150
CTCCAGATCG CAGCAATCGC GCCCCTATCT TGGCCCGCCC ACCTACTTAT 7200
GCAGGTATTC CCCGGGGTGC CATTAGTGGT TTTGTGGGCA AGTGGTTTGA 7250
CCGCAGTGGT TAGCGGGGTT ACAATCAGCC AAGTTATTAC ACCCTTATTT 7300
TACAGTCCAA AACCGCAGGG CGGCGTGTGG GGGCTGACGC GTGCCCCCAC 7350
TCCACAATTT CAAAAAAG AGTGGCCACT TGTCTTTGTT TATGGGCCCC 7400
ATTGGCGTGG AGCCCCGTTT AATTTTCGGG GGTGTTAGAG ACAACCAGTG 7450
GAGTCCGCTG CTGTCGGCGT CCACTCTCTT TCCCCTTGTT ACAAATAGAG 7500
TGTAACAACA TGGTTCACCT GTCTTGGTCC CTGCCTGGGA CACATCTTAA 7550
TAACCCCAAGT ATCATATTGC ACTAGGATTA TGTGTTGCCC ATAGCCATAA 7600
ATTCGTGTGA GATGGACATC CAGTCTTTAC GGCTTGTCCT CACCCCATGG 7650
ATTTCTATTG TTAAAGATAT TCAGAATGTT TCATTCCTAC ACTAGTATTT 7700
ATTGCCCAAG GGGTTTGTGA GGGTTATATT GGTGTCATAG CACAATGCCA 7750
CCACTGAACC CCCCGTCCAA ATTTTATTCT GGGGGCGTCA CCTGAAACCT 7800
TGTTTTCGAG CACCTCACAT ACACCTTACT GTTCACAACCT CAGCAGTTAT 7850
TCTATTAGCT AAACGAAGGA GAATGAAGAA GCAGGCGAAG ATTCAGGAGA 7900
GTTCACTGCC CGCTCCTTGA TCTTCAGCCA CTGCCCTTGT GACTAAAATG 7950
GTTCACTACC CTCGTGGAAT CCTGACCCCA TGTAATAAAA ACCGTGACAG 8000

CTCATGGGGT GGGAGATATC GCTGTTCCCTT AGGACCCTTT TACTAACCCT 8050
AATTCGATAG CATATGCTTC CCGTTGGGTA ACATATGCTA TTGAATTAGG 8100
GTTAGTCTGG ATAGTATATA CTA CTACTACCCG GGAAGCATAT GCTACCCGTT 8150
TAGGGTTAAC AAGGGGGCCT TATAAACACT ATTGCTAATG CCCTCTTGAG 8200
GGTCCGCTTA TCGGTAGCTA CACAGGCCCC TCTGATTGAC GTTGGTGTAG 8250
CCTCCCGTAG TCTTCCTGGG CCCCTGGGAG GTACATGTCC CCCAGCATTG 8300
GTGTAAGAGC TTCAGCCAAG AGTTACACAT AAAGGCAATG TTGTGTTGCA 8350
GTCCACAGAC TGCAAAGTCT GCTCCAGGAT GAAAGCCACT CAGTGTTGGC 8400
AAATGTGCAC ATCCATTTAT AAGGATGTCA ACTACAGTCA GAGAACCCCT 8450
TTGTGTTTGG TCCCCCCCCG TGTCACATGT GGAACAGGGC CCAGTTGGCA 8500
AGTTGTACCA ACCAACTGAA GGGATTACAT GCACTGCCCC 8540

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer UDEC690

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCCTGCAGG ACATCCAGAT GACTCAGTCT

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer UDEC395

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCAAGCTTA CTGGATGGTG GGAAGATGGA

30

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1M1 scFv (murine)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GCC GAC ATC CAG ATG ACT CAG TCT CCA 30

Met Ala Asp Ile Gln Met Thr Gln Ser Pro

1

5

10

GCT TCA CTG TCT GCA TCT GTG GGA GAA ACT 60
Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
15 20

GTC ACC ATC ACA TGT GGA GCA AGT GAG AAT 90
Val Thr Ile Thr Cys Gly Ala Ser Glu Asn
25 30

ATT TAC GGT GCT TTA AAT TGG TAT CAG CGG 120
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Arg
35 40

AAA CAG GGA AAA TCT CCT CAG CTC CTG ATC 150
Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
45 50

TAT GGT GCA ACC AAC TTG GCA GAT GGC ATG 180
Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met
55 60

TCA TCG AGG TTC AGT GGC AGT GGA TCT GGT 210
Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly
65 70

AGA CAG TAT TAT CTC AAG ATC AGT AGC CTG 240
Arg Gln Tyr Tyr Leu Lys Ile Ser Ser Leu
75 80

CAT CCT GAC GAT GTT GCA ACG TAT TAC TGT 270
His Pro Asp Asp Val Ala Thr Tyr Tyr Cys
85 90

CAA AAT GTG TTA AAT ACT CCT CTC ACG TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGT GCT GGG ACC AAG TTG GAG CTG AAA CGG 330
Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
105 110

ACC GGA GGT GGC GGG TCG GGT GGC GGG GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120

TCG GGT GGC GGA GGG TCG CAG GTT CAG CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
125 130

CAG CAG TCT GGA GCC GAG CTG ATG AAG CCT 420
Gln Gln Ser Gly Ala Glu Leu Met Lys Pro
135 140

GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT 450
Gly Ala Ser Val Lys Met Ser Cys Lys Ala
145 150

ACT GGC TAC ATA TTC AGT AAC TAC TGG ATA 480
Thr Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAG TGG ATA AAG CAG AGG CCT GGA CAT GGC 510
Gln Trp Ile Lys Gln Arg Pro Gly His Gly
165 170

CTT GAG TGG ATT GGT GAG ATT TTA CCT GGA 540
Leu Glu Trp Ile Gly Glu Ile Leu Pro Gly
175 180

AGT GGT TCT ACT GAG TAC ACT GAG AAC TTC 570
Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe
185 190

AAG GAC AAG GCC GCA TTC ACT GCA GAT ACA 600
Lys Asp Lys Ala Ala Phe Thr Ala Asp Thr
195 200

TCC TCC AAC ACA GCC TAC ATG CAA CTC AGC 630
Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser
205 210

AGC CTG ACA TCA GAG GAC TCT GCC GTC TAT 660
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
215 220

TAC TGT GCA AGA TAT TTC TTC GGT AGT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCC AAC TGG TAC TTC GAT GTC TGG GGC GCA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Ala
235 240

GGG ACC ACG GTC ACC GTC TCC TCA TGA 747
Gly Thr Thr Val Thr Val Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 scFv CB (humanized)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30

Met Ala Asp Ile Gln Met Thr Gln Ser Pro

1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

15 20

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 90

Val Thr Ile Thr Cys Gly Ala Ser Glu Asn

25 30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CGT 120

Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Arg

35 40

AAA CCT GGG AAA GCT CCG AAG CTT CTG ATT 150

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

45 50

TAC GGT GCG ACG AAC CTG GCA GAT GGA GTC 180

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val

55 60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly

65 70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu

75 80

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys

85 90

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
105 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
125 130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420
Val Gln Ser Gly Ala Glu Val Lys Lys Pro
135 140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450
Gly Ala Ser Val Lys Val Ser Cys Lys Ala
145 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly
165 170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540
Leu Glu Trp Met Gly Glu Ile Leu Pro Gly
175 180

TCT GGT AGC ACC GAA TAT ACC GAA AAT TTT 570
Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe
185 190

AAA GAC CGT GTT ACT ATG ACG CGT GAC ACT 600
Lys Asp Arg Val Thr Met Thr Arg Asp Thr
195 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
205 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747
Gly Thr Leu Val Thr Val Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION:5G1.1M1 VL HuK (chimeric light chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GGA ATC CAA GGA GGG TCT GTC CTG TTC 30
Met Gly Ile Gln Gly Gly Ser Val Leu Phe
-25 -20

GGG CTG CTG CTC GTC CTG GCT GTC TTC TGC 60
Gly Leu Leu Leu Val Leu Ala Val Phe Cys
-15 -10

CAT TCA GGT CAT AGC CTG CAG GAC ATC CAG 90
His Ser Gly His Ser Leu Gln Asp Ile Gln
-5 1 5

ATG ACT CAG TCT CCA GCT TCA CTG TCT GCA 120
Met Thr Gln Ser Pro Ala Ser Leu Ser Ala
10 15

TCT GTG GGA GAA ACT GTC ACC ATC ACA TGT 150
Ser Val Gly Glu Thr Val Thr Ile Thr Cys
20 25

GGA GCA AGT GAG AAT ATT TAC GGT GCT TTA 180
Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu
30 35

AAT TGG TAT CAG CGG AAA CAG GGA AAA TCT 210
Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser
40 45

CCT CAG CTC CTG ATC TAT GGT GCA ACC AAC 240
Pro Gln Leu Leu Ile Tyr Gly Ala Thr Asn
50 55

TTG GCA GAT GGC ATG TCA TCG AGG TTC AGT 270
Leu Ala Asp Gly Met Ser Ser Arg Phe Ser
60 65

GGC AGT GGA TCT GGT AGA CAG TAT TAT CTC 300
Gly Ser Gly Ser Gly Arg Gln Tyr Tyr Leu
70 75

AAG ATC AGT AGC CTG CAT CCT GAC GAT GTT 330
Lys Ile Ser Ser Leu His Pro Asp Asp Val
80 85

GCA ACG TAT TAC TGT CAA AAT GTG TTA AAT 360
Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn
90 95

ACT CCT CTC ACG TTC GGT GCT GGG ACC AAG 390
Thr Pro Leu Thr Phe Gly Ala Gly Thr Lys
100 105

TTG GAG CTG AAA CGA ACT GTG GCT GCA CCA 420
Leu Glu Leu Lys Arg Thr Val Ala Ala Pro
110 115

TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG 450
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
120 125

CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val
130 135

TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG 510
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
140 145

GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC 540
Ala Lys Val Gln Trp Lys Val Asp Asn Ala
150 155

CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC 570
Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
160 165

ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC 600
Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
170 175

AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA 630
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
180 185

GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC 660
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
190 195

TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG 690
Cys Glu Val Thr His Gln Gly Leu Ser Ser
200 205

CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG 720
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
210 215

TGT TAG 726
Cys

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid

135

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: 5G1.1M1 VH +HuG1 (chimeric Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG AAA TGG AGC TGG GTT ATT CTC TTC CTC 30
Met Lys Trp Ser Trp Val Ile Leu Phe Leu
-15 -10

CTG TCA GTA ACT GCA GGT GTC CAC TCC CAG 60
Leu Ser Val Thr Ala Gly Val His Ser Gln
-5 1

GTT CAG CTG CAG CAG TCT GGA GCT GAG CTG 90
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu
5 10

ATG AAG CCT GGG GCC TCA GTG AAG ATG TCC 120
Met Lys Pro Gly Ala Ser Val Lys Met Ser
15 20

TGC AAG GCT ACT GGC TAC ATA TTC AGT AAC 150
Cys Lys Ala Thr Gly Tyr Ile Phe Ser Asn
25 30

TAC TGG ATA CAG TGG ATA AAG CAG AGG CCT 180
Tyr Trp Ile Gln Trp Ile Lys Gln Arg Pro
35 40

GGA CAT GGC CTT GAG TGG ATT GGT GAG ATT 210
Gly His Gly Leu Glu Trp Ile Gly Glu Ile
45 50

TTA CCT GGA AGT GGT TCT ACT GAG TAC ACT 240
Leu Pro Gly Ser Gly Ser Thr Glu Tyr Thr
55 60

GAG AAC TTC AAG GAC AAG GCC GCA TTC ACT 270
Glu Asn Phe Lys Asp Lys Ala Ala Phe Thr
65 70

GCA GAT ACA TCC TCC AAC ACA GCC TAC ATG 300
Ala Asp Thr Ser Ser Asn Thr Ala Tyr Met
75 80

CAA CTC AGC AGC CTG ACA TCA GAG GAC TCT 330
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser
85 90

GCC GTC TAT TAC TGT GCA AGA TAT TTC TTC 360
Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe
95 100

GGT AGT AGC CCC AAC TGG TAC TTC GAT GTC 390
Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val
105 110

TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC 420
Trp Gly Ala Gly Thr Thr Val Thr Val Ser
115 120

TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC 450
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
125 130

CCC CTG GCG CCC TCC TCC AAG AGC ACC TCT 480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
135 140

GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC 510
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
145 150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
155 160

TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170

GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC 600
Val His Thr Phe Pro Ala Val Leu Gln Ser
175 180

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
185 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
195 200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690
Thr Tyr Ile Cys Asn Val Asn His Lys Pro
205 210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720
Ser Asn Thr Lys Val Asp Lys Lys Val Glu
215 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750
Pro Lys Ser Cys Asp Lys Thr His Thr
225

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 VH + IGHRL (Humanized Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30
Met Lys Trp Ser Trp Val Ile Leu Phe Leu
-15 -10

CTG TCA GTA ACT GCC GGC GTC CAC TCC CAA 60
Leu Ser Val Thr Ala Gly Val His Ser Gln
-5 1

GTC CAA CTG GTG CAA TCC GGC GCC GAG GTC 90
Val Gln Leu Val Gln Ser Gly Ala Glu Val
5 10

AAG AAG CCA GGG GCC TCA GTC AAA GTG TCC 120
Lys Lys Pro Gly Ala Ser Val Lys Val Ser
15 20

TGT AAA GCT AGC GGC TAT ATT TTT TCT AAT 150
Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn
25 30

TAT TGG ATT CAA TGG GTG CGT CAG GCC CCC 180
Tyr Trp Ile Gln Trp Val Arg Gln Ala Pro
35 40

GGG CAG GGC CTG GAA TGG ATG GGT GAG ATC 210
Gly Gln Gly Leu Glu Trp Met Gly Glu Ile
45 50

TTA CCG GGC TCT GGT AGC ACC GAA TAT GCC 240
Leu Pro Gly Ser Gly Ser Thr Glu Tyr Ala
55 60

CAA AAA TTC CAG GGC CGT GTT ACT ATG ACT 270
Gln Lys Phe Gln Gly Arg Val Thr Met Thr
65 70

GCG GAC ACT TCG ACT AGT ACA GCC TAC ATG 300
Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met
75 80

GAG CTC TCC AGC CTG CGA TCG GAG GAC ACG 330
Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
85 90

GCC GTC TAT TAT TGC GCG CGT TAT TTT TTT 360
Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe
95 100

GGT TCT AGC CCG AAT TGG TAT TTT GAT GTT 390
Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val
105 110

TGG GGT CAA GGA ACC CTG GTC ACT GTC TCG 420
Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120

AGC GCC TCC ACC AAG GGC CCA TCG GTC TTC 450
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
125 130

CCC CTG GCG CCC TCC TCC AAG AGC ACC TCT 480

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser

135

140

GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC 510

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val

145

150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

155

160

TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly

165

170

GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC 600

Val His Thr Phe Pro Ala Val Leu Gln Ser

175

180

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

185

190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln

195

200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690

Thr Tyr Ile Cys Asn Val Asn His Lys Pro

205

210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720

Ser Asn Thr Lys Val Asp Lys Lys Val Glu

215

220

141

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750

Pro Lys Ser Cys Asp Lys Thr His Thr

225

230

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION:5G1.1 VH + IGHRLC (Humanized Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30

Met Lys Trp Ser Trp Val Ile Leu Phe Leu

-15

-10

CTG TCA GTA ACT GCC GGC GTC CAC TCC CAA 60

Leu Ser Val Thr Ala Gly Val His Ser Gln

-5

1

GTC CAA CTG GTG CAA TCC GGC GCC GAG GTC 90

Val Gln Leu Val Gln Ser Gly Ala Glu Val

5

10

AAG AAG CCA GGG GCC TCA GTC AAA GTG TCC 120

Lys Lys Pro Gly Ala Ser Val Lys Val Ser

15

20

TGT AAA GCT AGC GGC TAT ATT TTT TCT AAT 150

Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn

25

30

TAT TGG ATT CAA TGG GTG CGT CAG GCC CCC 180

Tyr Trp Ile Gln Trp Val Arg Gln Ala Pro

35

40

GGG CAG GGC CTG GAA TGG ATG GGT GAG ATC 210

Gly Gln Gly Leu Glu Trp Met Gly Glu Ile

45

50

TTA CCG GGC TCT GGT AGC ACC GAA TAT ACC 240

Leu Pro Gly Ser Gly Ser Thr Glu Tyr Thr

55

60

GAA AAT TTT AAA GAC CGT GTT ACT ATG ACG 270

Glu Asn Phe Lys Asp Arg Val Thr Met Thr

65

70

CGT GAC ACT TCG ACT AGT ACA GTA TAC ATG 300

Arg Asp Thr Ser Thr Ser Thr Val Tyr Met

75

80

GAG CTC TCC AGC CTG CGA TCG GAG GAC ACG 330

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr

85

90

GCC GTC TAT TAT TGC GCG CGT TAT TTT TTT 360

Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe

95

100

GGT TCT AGC CCG AAT TGG TAT TTT GAT GTT 390

Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val

105

110

TGG GGT CAA GGA ACC CTG GTC ACT GTC TCG 420

Trp Gly Gln Gly Thr Leu Val Thr Val Ser

115

120

AGC GCC TCC ACC AAG GGC CCA TCG GTC TTC 450

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe

125

130

CCC CTG GCG CCC TCC TCC AAG AGC ACC TCT 480

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser

135

140

GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC 510

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val

145

150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

155

160

TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly

165

170

GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC 600

Val His Thr Phe Pro Ala Val Leu Gln Ser

175

180

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

185

190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln

195

200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690

Thr Tyr Ile Cys Asn Val Asn His Lys Pro

205

210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720

Ser Asn Thr Lys Val Asp Lys Lys Val Glu

215

220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750

Pro Lys Ser Cys Asp Lys Thr His Thr

225

230

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION:5G1.1 VL +KLV56

(Humanized light chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GGA ATC CAA GGA GGG TCT GTC CTG TTC 30

Met Gly Ile Gln Gly Gly Ser Val Leu Phe

-25

-20

GGG CTG CTG CTC GTC CTG GCT GTC TTC TGC 60

Gly Leu Leu Leu Val Leu Ala Val Phe Cys

-15

-10

CAT TCA GGT CAT AGC CTG CAG GAT ATC CAG 90

His Ser Gly His Ser Leu Gln Asp Ile Gln

-5

1

5

ATG ACC CAG TCC CCG TCC TCC CTG TCC GCC 120
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
10 15

TCT GTG GGC GAT AGG GTC ACC ATC ACC TGC 150
Ser Val Gly Asp Arg Val Thr Ile Thr Cys
20 25

GGC GCC AGC GAA AAC ATC TAT GGC GCG CTG 180
Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu
30 35

AAC TGG TAT CAA CGT AAA CCT GGG AAA GCT 210
Asn Trp Tyr Gln Arg Lys Pro Gly Lys Ala
40 45

CCG AAG CTT CTG ATT TAC GGT GCG ACG AAC 240
Pro Lys Leu Leu Ile Tyr Gly Ala Thr Asn
50 55

CTG GCA GAT GGA GTC CCT TCT CGC TTC TCT 270
Leu Ala Asp Gly Val Pro Ser Arg Phe Ser
60 65

GGA TCC GGC TCC GGA ACG GAT TAC ACT CTG 300
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
70 75

ACC ATC AGC AGT CTG CAA CCT GAG GAC TTC 330
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
80 85

GCT ACG TAT TAC TGT CAG AAC GTT TTA AAT 360
Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn
90 95

146

ACT CCG TTG ACT TTC GGA CAG GGT ACC AAG 390
Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys
100 105

GTG GAA ATA AAA CGA ACT GTG GCT GCA CCA 420
Val Glu Ile Lys Arg Thr Val Ala Ala Pro
110 115

TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG 450
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
120 125

CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val
130 135

TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG 510
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
140 145

GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC 540
Ala Lys Val Gln Trp Lys Val Asp Asn Ala
150 155

CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC 570
Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
160 165

ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC 600
Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
170 175

AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA 630
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
180 185

GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC 660
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
190 195

TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG 690
Cys Glu Val Thr His Gln Gly Leu Ser Ser
200 205

CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG 720
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
210 215

TGT TAG 726
Cys

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 VL +KLV56B
(Humanized light chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG GGA ATC CAA GGA GGG TCT GTC CTG TTC 30
Met Gly Ile Gln Gly Gly Ser Val Leu Phe
-25 -20

GGG CTG CTG CTC GTC CTG GCT GTC TTC TGC 60
Gly Leu Leu Leu Val Leu Ala Val Phe Cys
-15 -10

CAT TCA GGT CAT AGC CTG CAG GAT ATC CAG 90
His Ser Gly His Ser Leu Gln Asp Ile Gln
-5 1 5

ATG ACC CAG TCC CCG TCC TCC CTG TCC GCC 120
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
10 15

TCT GTG GGC GAT AGG GTC ACC ATC ACC TGC 150
Ser Val Gly Asp Arg Val Thr Ile Thr Cys
20 25

GGC GCC AGC GAA AAC ATC TAT GGC GCG CTG 180
Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu
30 35

AAC TGG TAT CAA CGT AAA CCT GGG AAA GCT 210
Asn Trp Tyr Gln Arg Lys Pro Gly Lys Ala
40 45

CCG AAG CTT CTG ATT TAC GGT GCG ACG AAC 240
Pro Lys Leu Leu Ile Tyr Gly Ala Thr Asn
50 55

CTG GCA GAT GGA GTC CCT TCT CGC TTC TCT 270
Leu Ala Asp Gly Val Pro Ser Arg Phe Ser
60 65

GGA TCC GGC TCC GGA ACG GAT TTC ACT CTG 300
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
70 75

ACC ATC AGC AGT CTG CAG CCT GAA GAC TTC 330
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
80 85

GCT ACG TAT TAC TGT CAG AAC GTT TTA AAT 360.

Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn

90

95

ACT CCG TTG ACT TTC GGA CAG GGT ACC AAG 390

Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys

100

105

GTG GAA ATA AAA CGA ACT GTG GCT GCA CCA 420

Val Glu Ile Lys Arg Thr Val Ala Ala Pro

110

115

TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG 450

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

120

125

CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG 480

Gln Leu Lys Ser Gly Thr Ala Ser Val Val

130

135

TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG 510

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu

140

145

GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC 540

Ala Lys Val Gln Trp Lys Val Asp Asn Ala

150

155

CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC 570

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val

160

165

ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC 600

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr

170

175

150

AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA 630

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys

180

185

GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC 660

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala

190

195

TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG 690

Cys Glu Val Thr His Gln Gly Leu Ser Ser

200

205

CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG 720

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu

210

215

TGT TAG

726

Cys

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION:5G1.1 VL + O12

(Humanized light chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATG GAC ATG AGG GTC CCC GCT CAG CTC CTG 30
Met Asp Met Arg Val Pro Ala Gln Leu Leu
-20 -15

GGG CTC CTG CTA CTC TGG CTC CGA GGT GCC 60
Gly Leu Leu Leu Leu Trp Leu Arg Gly Ala
-10 -5

AGA TGT GAT ATC CAG ATG ACC CAG TCC CCG 90
Arg Cys Asp Ile Gln Met Thr Gln Ser Pro
1 5

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 120
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
10 15

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 150
Val Thr Ile Thr Cys Gly Ala Ser Glu Asn
20 25

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 180
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln
30 35

AAA CCC GGG AAA GCT CCG AAG CTT CTG ATT 210
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
40 45

TAC GGT GCG ACG AAC CTG GCA GAT GGA GTC 240
Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val
50 55

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 270
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
60 65

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 300
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
70 75

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 330
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
80 85

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 360
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
90 95

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGA 390
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC 420
Thr Val Ala Ala Pro Ser Val Phe Ile Phe
110 115

CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA 450
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
120 125

ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC 480
Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135

TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG 510
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
140 145

AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC 540
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
150 155

TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC 570
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
160 165

AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC 600
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
170 175

CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA 630
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185

CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT 660
His Lys Val Tyr Ala Cys Glu Val Thr His
190 195

CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC 690
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
200 205

TTC AAC AGG GGA GAG TGT TAG 711
Phe Asn Arg Gly Glu Cys
210

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 VH + IGHRLD
(Humanized Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30
Met Lys Trp Ser Trp Val Ile Leu Phe Leu
-15 -10

CTG TCA GTA ACT GCC GGC GTC CAC TCC CAA 60
Leu Ser Val Thr Ala Gly Val His Ser Gln
-5 1

GTC CAA CTG GTG CAA TCC GGC GCC GAG GTC 90
Val Gln Leu Val Gln Ser Gly Ala Glu Val
5 10

AAG AAG CCA GGG GCC TCA GTC AAA GTG TCC 120
Lys Lys Pro Gly Ala Ser Val Lys Val Ser
15 20

TGT AAA GCT AGC GGC TAT ATT TTT TCT AAT 150
Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn
25 30

TAT TGG ATT CAA TGG GTG CGT CAG GCC CCC 180
Tyr Trp Ile Gln Trp Val Arg Gln Ala Pro
35 40

GGG CAG GGC CTG GAA TGG ATG GGT GAG ATC 210
Gly Gln Gly Leu Glu Trp Met Gly Glu Ile
45 50

TTA CCG GGC TCT GGT AGC ACC GAA TAT GCC 240
Leu Pro Gly Ser Gly Ser Thr Glu Tyr Ala
55 60

155

CAA AAA TTC CAG GGC CGT GTT ACT ATG ACT 270
Gln Lys Phe Gln Gly Arg Val Thr Met Thr
65 70

CGT GAC ACT TCG ACT AGT ACA GTA TAC ATG 300
Arg Asp Thr Ser Thr Ser Thr Val Tyr Met
75 80

GAG CTC TCC AGC CTG CGA TCG GAG GAC ACG 330
Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
85 90

GCC GTC TAT TAT TGC GCG CGT TAT TTT TTT 360
Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe
95 100

GGT TCT AGC CCG AAT TGG TAT TTT GAT GTT 390
Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val
105 110

TGG GGT CAA GGA ACC CTG GTC ACT GTC TCG 420
Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120

AGC GCC TCC ACC AAG GGC CCA TCG GTC TTC 450
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
125 130

CCC CTG GCG CCC TCC TCC AAG AGC ACC TCT 480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
135 140

GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC 510
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
145 150

150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
155 160

TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170

GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC 600
Val His Thr Phe Pro Ala Val Leu Gln Ser
175 180

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
185 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
195 200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690
Thr Tyr Ile Cys Asn Val Asn His Lys Pro
205 210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720
Ser Asn Thr Lys Val Asp Lys Lys Val Glu
215 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750
Pro Lys Ser Cys Asp Lys Thr His Thr
225 230

- (2) INFORMATION FOR SEQ ID NO:17:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: 5G1.1 scFv D012
(Humanized scFv)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30

Met Ala Asp Ile Gln Met Thr Gln Ser Pro

1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

15 20

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 90

Val Thr Ile Thr Cys Gly Ala Ser Glu Asn

25 30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120

Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln

35 40

AAA CCT GGG AAA GCT CCG AAG CTT CTG ATT 150

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

45 50

TAC GGT GCG ACG AAC CTG GCA GAT GGA GTC 180

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val

55 60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
65 70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
75 80

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
85 90

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
105 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
125 130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420
Val Gln Ser Gly Ala Glu Val Lys Lys Pro
135 140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450
Gly Ala Ser Val Lys Val Ser Cys Lys Ala
145 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly
165 170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540
Leu Glu Trp Met Gly Glu Ile Leu Pro Gly
175 180

TCT GGT AGC ACC GAA TAT GCC CAA AAA TTC 570
Ser Gly Ser Thr Glu Tyr Ala Gln Lys Phe
185 190

CAG GGC CGT GTT ACT ATG ACG CGT GAC ACT 600
Gln Gly Arg Val Thr Met Thr Arg Asp Thr
195 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
205 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747
Gly Thr Leu Val Thr Val Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5248 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: pET Trc S05/NI
prokaryotic expression vector

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG 50
TGTTACGCG CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT 100
CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GCTTTCCCCG 150
TCAAGCTCTA AATCGGGGGC TCCCTTTAGG GTTCCGATTT AGTGCTTTAC 200
GGCACCTCGA CCCCAAAAAA CTTGATTAGG GTGATGGTTC ACGTAGTGGG 250
CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT 300
CTTTAATAGT GGACTCTTGT TCCAAACTGG AACAACACTC AACCTATCT 350
CGGTCTATTC TTTTGATTTA TAAGGGATTT TGCCGATTTC GGCCTATTGG 400
TTAAAAAATG AGCTGATTTA ACAAAAATTT AACGCGAATT TTAACAAAAT 450

ATTAACGTTT ACAATTTTCAG GTGGCACTTT TCGGGGAAAT GTGCGCGGAA 500
CCCCTATTTG TTTATTTTTC TAAATACATT CAAATATGTA TCCGCTCATG 550
AGACAATAAC CCTGATAAAT GCTTCAATAA TATTGAAAAA GGAAGAGTAT 600
GAGTATTCAA CATTTCCGTG TCGCCCTTAT TCCCTTTTTT GCGGCATTTT 650
GCCTTCCTGT TTTTGCTCAC CCAGAAACGC TGGTGAAAGT AAAAGATGCT 700
GAAGATCAGT TGGGTGCACG AGTGGGTAC ATCGAACTGG ATCTCAACAG 750
CGGTAAGATC CTTGAGAGTT TTCGCCCGA AGAACGTTTT CCAATGATGA 800
GCACTTTTAA AGTTCTGCTA TGTGGCGCGG TATTATCCCG TATTGACGCC 850
GGGCAAGAGC AACTCGGTCG CCGCATAAC TATTCTCAGA ATGACTTGGT 900
TGAGTACTCA CCAGTCACAG AAAAGCATCT TACGGATGGC ATGACAGTAA 950
GAGAATTATG CAGTGCTGCC ATAACCATGA GTGATAACAC TGCGGCCAAC 1000
TACTTCTGA CAACGATCGG AGGACCGAAG GAGCTAACCG CTTTTTTGCA 1050
CAACATGGGG GATCATGTAA CTCGCCTTGA TCGTTGGGAA CCGGAGCTGA 1100
ATGAAGCCAT ACCAAACGAC GAGCGTGACA CCACGATGCC TGCAGCAATG 1150
GCAACAACGT TGCGCAAAC ATTAACCTGGC GAACTACTTA CTCTAGCTTC 1200
CCGGCAACAA TTAATAGACT GGATGGAGGC GGATAAAGTT GCAGGACCAC 1250
TTCTGCGCTC GGCCCTTCCG GCTGGCTGGT TTATTGCTGA TAAATCTGGA 1300
GCCGGTGAGC GTGGGTCTCG CGGTATCATT GCAGCACTGG GGCCAGATGG 1350

TAAGCCCTCC CGTATCGTAG TTATCTACAC GACGGGGAGT CAGGCAACTA 1400
TGGATGAACG AAATAGACAG ATCGCTGAGA TAGGTGCCTC ACTGATTAAG 1450
CATTGGTAAC TGTCAGACCA AGTTTACTCA TATATACTTT AGATTGATTT 1500
AAAACTTCAT TTTTAATTTA AAAGGATCTA GGTGAAGATC CTTTTTGATA 1550
ATCTCATGAC CAAAATCCCT TAACGTGAGT TTTCGTTCCA CTGAGCGTCA 1600
GACCCCGTAG AAAAGATCAA AGGATCTTCT TGAGATCCTT TTTTCTGCG 1650
CGTAATCTGC TGCTTGCAAA CAAAAAACC ACCGCTACCA GCGGTGGTTT 1700
GTTTGCCGGA TCAAGAGCTA CCAACTCTTT TTCCGAAGGT AACTGGCTTC 1750
AGCAGAGCGC AGATACCAA TACTGTCCTT CTAGTGTAGC CGTAGTTAGG 1800
CCACCACTTC AAGAACTCTG TAGCACC GCC TACATACCTC GCTCTGCTAA 1850
TCCTGTTACC AGTGGCTGCT GCCAGTGGCG ATAAGTCGTG TCTTACCGGG 1900
TTGGACTCAA GACGATAGTT ACCGGATAAG GCGCAGCGGT CGGGCTGAAC 1950
GGGGGGTTCG TGCACACAGC CCAGCTTGGA GCGAACGACC TACACCGAAC 2000
TGAGATACCT ACAGCGTGAG CTATGAGAAA GCGCCACGCT TCCCGAAGGG 2050
AGAAAGGCGG ACAGGTATCC GGTAAGCGGC AGGGTCGGAA CAGGAGAGCG 2100
CACGAGGGAG CTTCCAGGGG GAAACGCCTG GTATCTTTAT AGTCCTGTCTG 2150
GGTTTCGCCA CCTCTGACTT GAGCGTCGAT TTTTGTGATG CTCGTCAGGG 2200
GGGCGGAGCC TATGGAAAAA CGCCAGCAAC GCGGCCTTTT TACGGTTCCT 2250

GGCCTTTTGC TGGCCTTTTG CTCACATGTT CTTTCCTGCG TTATCCCCTG 2300
ATTCTGTGGA TAACCGTATT ACCGCCTTTG AGTGAGCTGA TACCGCTCGC 2350
CGCAGCCGAA CGACCGAGCG CAGCGAGTCA GTGAGCGAGG AAGCGGAAGA 2400
GCGCCTGATG CGGTATTTTC TCCTTACGCA TCTGTGCGGT ATTTACACACC 2450
GCATATATGG TGCACTCTCA GTACAATCTG CTCTGATGCC GCATAGTTAA 2500
GCCAGTATAC ACTCCGCTAT CGCTACGTGA CTGGGTCATG GCTGCGCCCC 2550
GACACCCGCC AACACCCGCT GACGCGCCCT GACGGGCTTG TCTGCTCCCG 2600
GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT GCATGTGTCA 2650
GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGGCAGCTG CGGTAAAGCT 2700
CATCAGCGTG GTCGTGAAGC GATTACAGA TGTCTGCCTG TTCATCCGCG 2750
TCCAGCTCGT TGAGTTTCTC CAGAAGCGTT AATGTCTGGC TTCTGATAAA 2800
GCGGGCCATG TTAAGGGCGG TTTTTTCCTG TTTGGTCACT GATGCCTCCG 2850
TGTAAGGGGG ATTTCTGTTC ATGGGGGTAA TGATACCGAT GAAACGAGAG 2900
AGGATGCTCA CGATACGGGT TACTGATGAT GAACATGCCC GGTTACTGGA 2950
ACGTTGTGAG GGTAAACAAC TGGCGGTATG GATGCGGCGG GACCAGAGAA 3000
AAATCACTCA GGGTCAATGC CAGCGCTTCG TTAATACAGA TGTAGGTGTT 3050
CCACAGGGTA GCCAGCAGCA TCCTGCGATG CAGATCCGGA ACATAATGGT 3100
GCAGGGCGCT GACTTCCGCG TTTCCAGACT TTACGAAACA CGGAAACCGA 3150

AGACCATTCA TGTGTGCT CAGGTCGCAG ACGTTTGTCA GCAGCAGTCG 3200
CTTCACGTTC GCTCGCGTAT CGGTGATTCA TTCTGCTAAC CAGTAAGGCA 3250
ACCCCGCCAG CCTAGCCGGG TCCTCAACGA CAGGAGCACG ATCATGCGCA 3300
CCCGTGGGGC CGCCATGCCG GCGATAATGG CCTGCTTCTC GCCGAAACGT 3350
TTGGTGGCGG GACCAGTGAC GAAGGCTTGA GCGAGGGCGT GCAAGATTCC 3400
GAATACCGCA AGCGACAGGC CGATCATCGT CGCGCTCCAG CGAAAGCGGT 3450
CCTCGCCGAA AATGACCCAG AGCGCTGCCG GCACCTGTCC TACGAGTTGC 3500
ATGATAAAGA AGACAGTCAT AAGTGCGGCG ACGATAGTCA TGCCCCGCGC 3550
CCACCGGAAG GAGCTGACTG GGTGAAGGC TCTCAAGGGC ATCGGTTCGAG 3600
ATCCCGGTGC CTAATGAGTG AGCTAACTTA CATTAATTGC GTTGCGCTCA 3650
CTGCCCCGCTT TCCAGTCGGG AAACCTGTCTG TGCCAGCTGC ATTAATGAAT 3700
CGGCCAACGC GCGGGGAGAG GCGGTTTGCG TATTGGGCGC CAGGGTGGTT 3750
TTTCTTTTCA CCAGTGAGAC GGGCAACAGC TGATTGCCCT TCACCGCCTG 3800
GCCCTGAGAG AGTTGCAGCA AGCGGTCCAC GCTGGTTTGC CCCAGCAGGC 3850
GAAAATCCTG TTTGATGGTG GTTAACGGCG GGATATAACA TGAGCTGTCT 3900
TCGGTATCGT CGTATCCCAC TACCGAGATA TCCGCACCAA CGCGCAGCCC 3950
GGA CTCGGTA ATGGCGCGCA TTGCGCCCAG CGCCATCTGA TCGTTGGCAA 4000
CCAGCATCGC AGTGGGAACG ATGCCCTCAT TCAGCATTTG CATGGTTTGT 4050

TGAAAACCGG ACATGGCACT CCAGTCGCCT TCCCGTTCCG CTATCGGCTG 4100
AATTTGATTG CGAGTGAGAT ATTTATGCCA GCCAGCCAGA CGCAGACGCG 4150
CCGAGACAGA ACTTAATGGG CCCGCTAACA GCGCGATTTG CTGGTGACCC 4200
AATGCGACCA GATGCTCCAC GCCCAGTCGC GTACCGTCTT CATGGGAGAA 4250
AATAATACTG TTGATGGGTG TCTGGTCAGA GACATCAAGA AATAACGCCG 4300
GAACATTAGT GCAGGCAGCT TCCACAGCAA TGGCATCCTG GTCATCCAGC 4350
GGATAGTTAA TGATCAGCCC ACTGACGCGT TGC GCGAGAA GATTGTGCAC 4400
CGCCGCTTTA CAGGCTTCGA CGCCGCTTCG TTCTACCATC GACACCACCA 4450
CGCTGGCACC CAGTTGATCG GCGCGAGATT TAATCGCCGC GACAATTTGC 4500
GACGGCGCGT GCAGGGCCAG ACTGGAGGTG GCAACGCCAA TCAGCAACGA 4550
CTGTTTGCCC GCCAGTTGTT GTGCCACGCG GTTGGGAATG TAATTCAGCT 4600
CCGCCATCGC CGCTTCCACT TTTTCCCGCG TTTTCGCAGA AACGTGGCTG 4650
GCCTGGTTCA CCACGCGGGA AACGGTCTGA TAAGAGACAC CGGCATACTC 4700
TGCGACATCG TATAACGTTA CTGGTTTCAC ATTCACCACC CTGAATTGAC 4750
TCTCTTCCGG GCGCTATCAT GCCATACCGC GAAAGGTTTT GCGCCATTCG 4800
ATGGTGTCCG GGATCTCGAC GCTCTCCCTT ATGCGACTCC TGCATTAGGA 4850
AGCAGCCCAG TAGTAGGTTG AGGCCGTTGA GCACCGCCGC CGCAAGGAAT 4900
GGTG CATGCG GTACCAGCTG TTGACAATTA ATCATCCGGC TCGTATAATA 4950

GTACTGTGTG GAATTGTGAG CGCTCACAAT TCCACACATC TAGAAATAAT 5000
TTTGTTTAAC TTTAAGAAGG AGATATACCA TGGAGATCTG GATCCATCGA 5050
TGAATTCGAG CTCCGTCGAC AAGCTTGCGG CCGCACTCGA GCACCACCAC 5100
CACCACCACT GAGATCCGGC TGCTAACAAA GCCCGAAAGG AAGCTGAGTT 5150
GGCTGCTGCC ACCGCTGAGC AATAACTAGC ATAACCCCTT GGGGCCTCTA 5200
AACGGGTCTT GAGGGGTTTT TTGCTGAAAG GAGGAACTAT ATCCGGAT 5248

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: N19/8 scFv (His Tagged)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG GCC AAT ATT GTG CTG ACC CAA TCT CCA 30

Met Ala Asn Ile Val Leu Thr Gln Ser Pro

1 5 10

GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG 60

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg

15 20

GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT 120

Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser

25 30

GTT GAT AGT TAT GAC AAT AGT TTT ATG CAC 150

Val Asp Ser Tyr Asp Asn Ser Phe Met His

35

40

TGG TAC CAG CAG AAA CCA GGA CAG CCA CCC 180

Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro

45

50

AAA CTC CTC ATC TTT CTT GCA TCC AAC CTA 210

Lys Leu Leu Ile Phe Leu Ala Ser Asn Leu

55

60

GAA TCT GGG GTC CCT GCC AGG TTC AGT GGC 240

Glu Ser Gly Val Pro Ala Arg Phe Ser Gly

65

70

AGT GGG TCT AGG ACA GAC TTC ACC CTC ACC 270

Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr

75

80

ATT GAT CCT GTG GAG GCT GAT GAT GCT GCA 300

Ile Asp Pro Val Glu Ala Asp Asp Ala Ala

85

90

ACC TAT TAC TGT CAG CAA AAT AAT GAG GTT 330

Thr Tyr Tyr Cys Gln Gln Asn Asn Glu Val

95

100

CCG AAC ACG TTC GGA GGG GGG ACC AAG CTG 360

Pro Asn Thr Phe Gly Gly Gly Thr Lys Leu

105

110

GAA ATA AAA CGG ACC GGA GGT GGC GGG TCG 390

Glu Ile Lys Arg Thr Gly Gly Gly Gly Ser

115

120

GGT GGC GGG GGA TCG GGT GGC GGA GGG TCG 420
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
125 130

GAC GTC AAG CTC GTG GAG TCT GGG GGA GAC 450
Asp Val Lys Leu Val Glu Ser Gly Gly Asp
135 140

TTA GTG AAG CTT GGA GGG TCC CTG AAA CTC 480
Leu Val Lys Leu Gly Gly Ser Leu Lys Leu
145 150

TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT 510
Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
155 160

AGC TAT TAT ATG TCT TGG GTT CGC CAG ATT 540
Ser Tyr Tyr Met Ser Trp Val Arg Gln Ile
165 170

TCA GAG AAG AGG CTG GAG TTG GTC GCA GCC 570
Ser Glu Lys Arg Leu Glu Leu Val Ala Ala
175 180

ATT AAT AGT AAT GGT GAT AGC ACC TAC TAT 600
Ile Asn Ser Asn Gly Asp Ser Thr Tyr Tyr
185 190

CCA GAC ACT GTG AAG GGC CGA TTC ACC ATC 630
Pro Asp Thr Val Lys Gly Arg Phe Thr Ile
195 200

TCC AGA GAC AAT GCC AAG AGC ACC CTG GAT 660
Ser Arg Asp Asn Ala Lys Ser Thr Leu Asp
205 210

CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC 690

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp

215

220

ACA GCC TTG TAT TTC TGT GTA AGA GAG ACT 720

Thr Ala Leu Tyr Phe Cys Val Arg Glu Thr

225

230

TAT TAC TAC GGG ATT AGT CCC GTC TTC GAT 750

Tyr Tyr Tyr Gly Ile Ser Pro Val Phe Asp

235

240

GTC TGG GGC ACA GGG ACC ACG GTC ACC GTC 780

Val Trp Gly Thr Gly Thr Thr Val Thr Val

245

250

TCC TCA CTC GAG CAC CAC CAC CAC CAC CAC 810

Ser Ser Leu Glu His His His His His His

255

260

TGA

813

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: 5G1.1 scFv C012 (humanized)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG	GCC	GAT	ATC	CAG	ATG	ACC	CAG	TCC	CCG	30
Met	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	
1				5					10	
TCC	TCC	CTG	TCC	GCC	TCT	GTG	GGC	GAT	AGG	60
Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
				15					20	
GTC	ACC	ATC	ACC	TGC	GGC	GCC	AGC	GAA	AAC	90
Val	Thr	Ile	Thr	Cys	Gly	Ala	Ser	Glu	Asn	
				25					30	
ATC	TAT	GGC	GCG	CTG	AAC	TGG	TAT	CAA	CAG	120
Ile	Tyr	Gly	Ala	Leu	Asn	Trp	Tyr	Gln	Gln	
				35					40	
AAA	CCC	GGG	AAA	GCT	CCG	AAG	CTT	CTG	ATT	150
Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
				45					50	
TAC	GGT	GCG	ACG	AAC	CTG	GCA	GAT	GGA	GTC	180
Tyr	Gly	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Val	
				55					60	
CCT	TCT	CGC	TTC	TCT	GGA	TCC	GGC	TCC	GGA	210
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
				65					70	
ACG	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	CTG	240
Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
				75					80	
CAG	CCT	GAA	GAC	TTC	GCT	ACG	TAT	TAC	TGT	270
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
				85					90	

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
105 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
125 130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420
Val Gln Ser Gly Ala Glu Val Lys Lys Pro
135 140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450
Gly Ala Ser Val Lys Val Ser Cys Lys Ala
145 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly
165 170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540
Leu Glu Trp Met Gly Glu Ile Leu Pro Gly
175 180

TCT GGT AGC ACC GAA TAT ACC GAA AAT TTT 570
Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe
185 190

AAA GAC CGT GTT ACT ATG ACG CGT GAC ACT 600
Lys Asp Arg Val Thr Met Thr Arg Asp Thr
195 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
205 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747
Gly Thr Leu Val Thr Val Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

173

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: 5G1.1 scFv D012B

(Humanized scFv)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30

Met Ala Asp Ile Gln Met Thr Gln Ser Pro

1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

15 20

GTC ACC ATC ACC TGC CGT GCT AGC GAA AAC 90

Val Thr Ile Thr Cys Arg Ala Ser Glu Asn

25 30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120

Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln

35 40

AAA CCT GGG AAA GCT CCG AAG CTT CTG ATT 150

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

45 50

TAC GGT GCG ACG AAC CTG GCA GAT GGA GTC 180

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val

55 60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly

65 70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
75 80

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
85 90

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
105 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
125 130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420
Val Gln Ser Gly Ala Glu Val Lys Lys Pro
135 140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450
Gly Ala Ser Val Lys Val Ser Cys Lys Ala
145 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly
165 170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540
Leu Glu Trp Met Gly Glu Ile Leu Pro Gly
175 180

TCT GGT AGC ACC GAA TAT GCC CAA AAA TTC 570
Ser Gly Ser Thr Glu Tyr Ala Gln Lys Phe
185 190

CAG GGC CGT GTT ACT ATG ACG CGT GAC ACT 600
Gln Gly Arg Val Thr Met Thr Arg Asp Thr
195 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
205 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747
Gly Thr Leu Val Thr Val Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: 5G1.1 scFv D012C
(Humanized scFv)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30

Met Ala Asp Ile Gln Met Thr Gln Ser Pro

1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

15 20

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 90

Val Thr Ile Thr Cys Gly Ala Ser Glu Asn

25 30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120

Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln

35 40

AAA CCT GGG AAA GCT CCG AAG CTT CTG ATT 150

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

45 50

TAC GGT GCG ACG AGC CTG CAG TCT GGA GTC 180
Tyr Gly Ala Thr Ser Leu Gln Ser Gly Val
55 60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
65 70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
75 80

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
85 90

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
105 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
125 130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420
Val Gln Ser Gly Ala Glu Val Lys Lys Pro
135 140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450
Gly Ala Ser Val Lys Val Ser Cys Lys Ala
145 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly
165 170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540
Leu Glu Trp Met Gly Glu Ile Leu Pro Gly
175 180

TCT GGT AGC ACC GAA TAT GCC CAA AAA TTC 570
Ser Gly Ser Thr Glu Tyr Ala Gln Lys Phe
185 190

CAG GGC CGT GTT ACT ATG ACG CGT GAC ACT 600
Gln Gly Arg Val Thr Met Thr Arg Asp Thr
195 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
205 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747
Gly Thr Leu Val Thr Val Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 scFv D012D
(Humanized scFv)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30
Met Ala Asp Ile Gln Met Thr Gln Ser Pro
1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
15 20

GTC ACC ATC ACC TGC CGT GCT AGC GAA AAC 90
Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
25 30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln
35 40

AAA CCT GGG AAA GCT CCG AAG CTT CTG ATT 150
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
45 50

TAC GGT GCG ACG AGC CTG CAG TCT GGA GTC 180
Tyr Gly Ala Thr Ser Leu Gln Ser Gly Val
55 60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
65 70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
75 80

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
85 90

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
105 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
125 130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420
Val Gln Ser Gly Ala Glu Val Lys Lys Pro
135 140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450
Gly Ala Ser Val Lys Val Ser Cys Lys Ala
145 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly
165 170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540
Leu Glu Trp Met Gly Glu Ile Leu Pro Gly
175 180

TCT GGT AGC ACC GAA TAT GCC CAA AAA TTC 570
Ser Gly Ser Thr Glu Tyr Ala Gln Lys Phe
185 190

CAG GGC CGT GTT ACT ATG ACG CGT GAC ACT 600
Gln Gly Arg Val Thr Met Thr Arg Asp Thr
195 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
205 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747
Gly Thr Leu Val Thr Val Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 scFv C013 (humanized)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30
Met Ala Asp Ile Gln Met Thr Gln Ser Pro
1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
15 20

GTC ACC ATC ACC TGC CGT GCT AGC GAA AAC 90
Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
25 30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln
35 40

AAA CCC GGG AAA GCT CCG AAG CTT CTG ATT 150
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
45 50

TAC GGT GCG ACG AAC CTG GCA GAT GGA GTC 180
Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val
55 60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
65 70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
75 80

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
85 90

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

105

110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360

Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly

115

120

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu

125

130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420

Val Gln Ser Gly Ala Glu Val Lys Lys Pro

135

140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450

Gly Ala Ser Val Lys Val Ser Cys Lys Ala

145

150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480

Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile

155

160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510

Gln Trp Val Arg Gln Ala Pro Gly Gln Gly

165

170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540

Leu Glu Trp Met Gly Glu Ile Leu Pro Gly

175

180

TCT GGT AGC ACC GAA TAT ACC GAA AAT TTT 570

Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe

185

190

AAA GAC CGT GTT ACT ATG ACG CGT GAC ACT 600

Lys Asp Arg Val Thr Met Thr Arg Asp Thr

195	200
TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630	
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser	
205	210
AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660	
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr	
215	220
TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690	
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser	
225	230
CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720	
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln	
235	240
GGA ACC CTG GTC ACT GTC TCG AGC TGA 747	
Gly Thr Leu Val Thr Val Ser Ser	
245	

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 scFv C014 (humanized)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

96

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30
Met Ala Asp Ile Gln Met Thr Gln Ser Pro
1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
15 20

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 90
Val Thr Ile Thr Cys Gly Ala Ser Glu Asn
25 30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln
35 40

AAA CCC GGG AAA GCT CCG AAG CTT CTG ATT 150
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
45 50

TAC GGT GCG ACG AGC CTG CAG TCT GGA GTC 180
Tyr Gly Ala Thr Ser Leu Gln Ser Gly Val
55 60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
65 70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
75 80

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
85 90

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300

Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
105 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
125 130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420
Val Gln Ser Gly Ala Glu Val Lys Lys Pro
135 140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450
Gly Ala Ser Val Lys Val Ser Cys Lys Ala
145 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly
165 170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540
Leu Glu Trp Met Gly Glu Ile Leu Pro Gly
175 180

TCT GGT AGC ACC GAA TAT ACC GAA AAT TTT 570

Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe
185 190

AAA GAC CGT GTT ACT ATG ACG CGT GAC ACT 600
Lys Asp Arg Val Thr Met Thr Arg Asp Thr
195 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
205 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747
Gly Thr Leu Val Thr Val Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

189

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: 5G1.1 scFv C015 (humanized)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30

Met Ala Asp Ile Gln Met Thr Gln Ser Pro

1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

15 20

GTC ACC ATC ACC TGC CGT GCT AGC GAA AAC 90

Val Thr Ile Thr Cys Arg Ala Ser Glu Asn

25 30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120

Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln

35 40

AAA CCC GGG AAA GCT CCG AAG CTT CTG ATT 150

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

45 50

TAC GGT GCG ACG AGC CTG CAG TCT GGA GTC 180

Tyr Gly Ala Thr Ser Leu Gln Ser Gly Val

55 60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly

65 70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu

75 80

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
85 90

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
105 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
125 130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420
Val Gln Ser Gly Ala Glu Val Lys Lys Pro
135 140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450
Gly Ala Ser Val Lys Val Ser Cys Lys Ala
145 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly
165 170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540
Leu Glu Trp Met Gly Glu Ile Leu Pro Gly
175 180

TCT GGT AGC ACC GAA TAT ACC GAA AAT TTT 570
Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe
185 190

AAA GAC CGT GTT ACT ATG ACG CGT GAC ACT 600
Lys Asp Arg Val Thr Met Thr Arg Asp Thr
195 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
205 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747
Gly Thr Leu Val Thr Val Ser Ser
245